Journal of Spices and Aromatic Crops
Vol. 22 (1) : 85–87 (2013)
www.indianspicesociety.in/josac/index.php/josac

Indian Society for Spices

Genetic evaluation for biometrical traits in fennel (*Foeniculum vulgare* Mill.)

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Received 28 December 2011; Revised 30 April 2012; Accepted 23 July 2012

Abstract

The genetic variability, heritability, genetic advance, phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) of 13 diverse genotypes of fennel were studied. Considerable amount of variation were recorded for all the characters. The phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) in all the characters. The maximum genotypic coefficient of variation (GCV) was recorded for yield plant^{-1} (40.27) followed by seed yield (32.40 q ha^{-1}), weight of seed umbel^{-1} (27.12), number of umbellets umbel^{-1} (17.47) and number of seeds umbel^{-1} (16.88). High heritability coupled with high genetic advance were recorded for number of seeds umbel^{-1}, yield plant^{-1}, plant height, number of umbel plant^{-1} and number of branches plant^{-1}.

Keywords: *Foeniculum vulgare*, fennel, genetic evaluation

Improvement in any crop depends on the magnitude of genetic variability and the degree of transmission of characters from one generation to the next. Besides, the knowledge of association between yield and its contributing traits will be of great value in planning a breeding programme. Genotypic and phenotypic coefficient of variation help to access the divergence of those traits which exhibit high variability along with moderate to high genetic gain for making selection of fennel for which very little information is available. Therefore, effort was made to investigate the extent of genetic variability to access the interaction among the twelve characters and to understand the nature of direct and indirect effect of those characters on yield.

The present experiment was carried out at Horticulture Research Farm, Department of Applied Plant Science (Horticulture), Babasaheb Bhimrao Ambedkar University, Lucknow U.P. The experimental materials comprised of 13 genotypes. The experiment was laid out in Randomized Block Design (RBD) with three replications during the year 2011. The row to row and plant to plant spacing were maintained at 45 cm × 25 cm, respectively. Recommended package of practices were followed. Observations were recorded from five randomly selected plants taken from each plot for twelve quantitative characters *viz*., Days to

50% germination, plant height, number of branches plant^{-1}, days to 50% flowering, number of umbel plant^{-1}, number of umbellets umbel^{-1}, days to maturity, 1000-seed weight, weight of seed umbel^{-1}, yield plant^{-1} and seed yield. The analysis of variance and genetic variability were calculated as per methods suggested by Panse & Sukhatme (1978). The phenotypic and genotypic coefficient of variation (PCV and GCV respectively) were calculated as per the model of Burton & Devane (1953). Heritability estimates and genetic advance (percent of mean) were calculated by the methods of Hanson *et al.* (1956) and Johnson *et al.* (1955a) respectively.

Analysis of variance revealed that mean sum of square due to variance was significant for all the characters (Table 1). The extent of variability measured in terms of range, mean GCV, PCV, heritability and genetic advance are given in Table 1. The coefficient of variation were less than 20% for all the characters confirming the reliability of the experiment and also suggesting less G × E interactions. PCV was close to GCV but the magnitude of PCV was more than GCV for most of the characters. In the present experiment, maximum GCV and PCV (Table 1) were recorded for the characters like yield plant^{-1}, seed yield (q ha^{-1}), weight of seed umbel^{-1}, number of umbellets umbel^{-1}, number of seeds umbel^{-1}, number of umbels plant^{-1} and number of branches plant^{-1}. High heritability was recorded in characters like yield plant^{-1} followed by weight of seed umbel^{-1}, number of branches plant^{-1}, 1000-seed weight, seed yield, number of umbel plant^{-1}, number of umbellets umbel^{-1} and number of umbel plant^{-1}, number of umbellets umbel^{-1} and number of seed umbel^{-1}. Moderate heritability was recorded for days to 50% germination, days to 50% flowering and plant height, while, least was recorded in days to maturity. High heritability in broad sense indicated that large proportion of PCV was attributed to the GCV and the characters different among the genotypes were real and genetic in nature with less influence of environment and such traits are considered dependable from breeding point of view and selection based on phenotypic

Table 1. Estimation of analysis of variance (replication, treatment & error), range, general mean, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance for various characters in fennel

Characters	Replications	Treatments	Error	Range		General mean	GCV (%)	PCV (%)	Heritability (%)	Genetic advance
				Minimum	Maximum					
	2	12	24							
Days to germination	75.53	70.25**	87.29	9.61	13.25	11.88	7.18	8.47	71.80	1.49
Plant height (cm)	73.47	95.13**	40.49	97.02	123.43	108.65	7.43	9.19	65.30	13.43
Number of branches plant^{-1}	0.83	10.38**	10.53	30.66	49.24	39.99	12.27	12.85	91.20	9.65
Days to 50% flowering	0.11	30.61**	9.18	86.81	105.33	93.81	9.72	6.87	69.40	9.21
Number of umbels plant^{-1}	0.02	28.35**	3.75	31.01	50.25	41.05	13.86	14.90	86.50	10.90
Number of umbellets umbel^{-1}	10.13	75.32**	0.22	18.41	32.04	23.87	17.47	18.79	86.40	7.98
Number of seeds umbel^{-1}	0.13	95.11**	0.13	442.33	742.33	604.92	16.88	18.35	84.60	193.56
Days to maturity	0.17	1.56**	1.31	219.89	229.89	222.51	1.16	1.84	39.60	3.34
1000-seed Wt.(g)	0.65	0.24**	7.14	4.38	6.07	5.02	10.03	10.53	90.80	0.99
Weight of seed umbel^{-1}	0.86	0.19**	5.76	0.58	1.52	0.88	27.12	27.89	94.60	0.48
Yield plant^{-1}	100.81	121.49**	19.42	17.89	98.31	64.30	40.27	40.93	96.80	52.47
Seed yield (q ha^{-1})	20.33	85.48**	0.85	8.65	15.69	11.36	32.40	34.55	88.00	7.11

*, ** Significant at 5% and 1%, respectively

expression could be relied upon. Heritability and genetic advance are important selection parameters. Heritability estimates along with genetic advance are normally more useful in predicting the gain under than heritability estimate alone. However, it is not necessary that a characters showing high heritability will also exhibit high genetic advance. Estimates of heritability also give some idea about the gene action involved in the various polygenetic traits (Johnson *et al.* 1955b). High expected genetic advance were observed for number of seed umbel^{-1} followed by yield plant^{-1}, plant height, number of umbel plant^{-1} and number of primary branches plant^{-1} along with high heritability estimates. Thus, it could be inferred that the most of the traits *viz*., number of seed umbel^{-1}, yield plant^{-1}, plant height, number of umbel plant^{-1} and number of primary branches plant^{-1} are under additive gene effects and hence, selection for these traits may result in improvement of superior genotypes in fennel.

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